AMENDMENT

In the Specification:

Please replace the paragraph on page 12 lines 9-21 with the following:

The term "x% homology" refers to the extent to which two nucleic acid or protein sequences are complementary as determined by BLAST homology alignment as described by T.A. Tatusova & T.L. Madden (1999), "Blast 2 sequences - a new tool for comparing protein and nucleotide sequences", FEMS MICROBIOL LETT. **174**:247-250 and using the following

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parameters: Program (blastn) or (blastp) as appropriate; matrix (OBLOSUM62), reward for match (1); penalty for mismatch (-2); open gap (5) and extension gap (2) penalties; gap x- drop off (50); Expect (10); word size (11); filter (off). An example of a web based two sequence alignment program using these parameters is found at the world wide web address:ncbi.nlm.nih.gov/gorf/bl2.html.

In the Claims:

Please replace the presently pending claims with the following claims:

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13. (Amended) A method to design primers to target a first nucleotide sequence that results in at least one phenotypic characteristic, the method comprising the steps of:

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providing a second nucleotide sequence that is known to result in the phenotypic characteristic;

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comparing the second nucleotide sequence to nucleotide sequences cataloged in one or more databases that correlate nucleotide sequences with phenotypic characteristics;

extracting any cataloged gene sequences that contain a portion of the second nucleotide sequence and which result in said phenotypic characteristic;

aligning the second nucleotide sequence to each extracted gene sequence;

prioritizing the extracted gene sequences to ensure alignment to the second nucleotide sequence; and

designing one or more primers based on matching portions of the alleged prioritized sequences to target said first nucleotide sequence.

14. (Amended) The method of claim 13, further comprising the step of filtering the extracted nucleotide sequences to eliminate portions common to unwanted genes.

15. (Amended) The method of claim 14, wherein the step of filtering the extracted nucleotide sequences removes vertebrate sequences but not invertebrate derived sequences.

16. (Amended) The method of claim 13, further comprising the step of cloning genetic material using the one or more designed primers.

17. (Amended) The method of claim 13, wherein the one or more databases are selected from cataloged sequences for humans, rats, mice, zebra fish, frogs, Drosophila, nematode, C. elegans, mosquito and bacteria.

18. (Amended) The method of claim 13, wherein said phenotypic characteristic is expression in insect mid-gut epithelium.

19. (Amended) The method of claim 13, wherein the one or more primers are nested.

Please cancel claims 20-22.

23. (Amended) The method of claim 13, wherein the step of prioritizing the extracted nucleotide sequences to ensure the alignment of the selected nucleotide sequences is accomplished by using a statistical analysis of the alignment.

Please cancel claim 24.

25. (Amended) The method of claim 13, wherein the second nucleotide sequence is aligned to each extracted nucleotide sequence by comparing deduced amino acid sequences.

26. (Amended) The method of claim 13, wherein the second nucleotide sequence is aligned to each extracted nucleotide sequence by comparing the nucleotide sequences.

Please cancel claims 27-33.

34. (Amended) A system for designing primers to target a first nucleotide sequence that results in at least one phenotypic characteristic comprising:

one or more computers collectively having program means thereon for performing the method of claim 1; and

one or more databases containing the cataloged gene sequences; and

a communication link connecting the computer or computers to said one or more databases.

Please cancel claim 35.

36. (Amended) The system of claim 34, wherein the program means filters the extracted nucleotide sequences to eliminate portions common to unwanted genes.

37. (Amended) The system of claim 36, wherein the program means removes vertebrate sequences but not invertebrate derived sequences when the sequences are filtered.

38. (Amended) The system of claim 36, further comprising an apparatus that clones genetic material using one or more primers.

39. (Amended) The system of claim 36, wherein the one or more databases are selected from cataloged gene sequences for humans, rats, mice, zebra fish, frogs, Drosophila, nematode, C. elegans, mosquito and bacteria.

40. (Amended) The system of claim 36, wherein the phenotypic characteristic is expression in insect mid-gut epithelium.

41. (Amended) The system of claim 36, wherein the one or more primers are nested.

Please cancel claims 42-44.

45. (Amended) The system of claim 36, wherein the program means uses a statistical analysis of the alignment of the second nucleotide sequence to prioritize the extracted sequences.

Please cancel claim 46.

47. (Amended) The system of claim 36, wherein the selected gene sequence is aligned to each extracted nucleotide sequence by comparing deduced amino acid sequences.

48. (Amended) The system of claim 36, wherein the second nucleotide sequence is aligned to each extracted gene sequence by comparing nucleotide sequences.

Please cancel claims 49-59.

60. (Amended) A computer program embodied on a computer-readable medium for designing primers to target a first nucleotide sequence that results in at least one phenotypic characteristic, said computer program comprising:

means for providing a second nucleotide sequence that results in the phenotypic characteristic;

means for providing at least one database containing cataloged nucleotide sequences therein wherein said catalog correlates sequence to resulting phenotypic characteristics;

means for extracting from said at least one database a plurality of cataloged nucleotide sequences containing a portion of the said second nucleotide sequence;

means for aligning said second nucleotide sequence with said cataloged gene sequences;

means for prioritizing the extracted gene sequences to ensure alignment with the second nucleotide sequence; and

means for designing one or more primers based on matching portions of the aligned prioritized sequences to target said first nucleotide sequence.

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61. (Amended) The computer program of claim 60, further comprising a code segment for filtering the extracted nucleotide sequences.

62. (Amended) The computer program of claim 61, wherein the code segment for filtering the prioritized gene sequences removes vertebrate sequences but not invertebrate derived sequences.

Please cancel claim 63.

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64. (Amended) The computer program of claim 60, wherein the one or more databases are selected from cataloged gene sequences for humans, rats, mice, zebra fish, frogs, Drosophila, nematode, C. elegans, mosquito and bacteria.

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65. (Amended) The computer program of claim 60, wherein the phenotypic characteristic is expression in insect mid-gut epithelium.

66. (Amended) The computer program of claim 60, wherein the one or more primers are nested.

Please cancel claims 67-69.

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70. (Amended) The computer program of claim 60, wherein the code segment for prioritizing the extracted nucleotide sequences based on alignment with the second nucleotide sequence is accomplished by using a statistical analysis of the alignment.

Please cancel claim 71.

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72. (Amended) The computer program of claim 60, wherein the second nucleotide sequence is aligned to each extracted nucleotide sequence by comparing deduced amino acid sequences.

73. (Amended) The computer program of claim 60, wherein the second nucleotide sequence is aligned to each extracted nucleotide sequence by comparing deduced nucleic acid sequences.

Please cancel claims 74-80.

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81. (Amended) An article of manufacture comprising a computer medium having computer readable program code means of claim 60 embodied therein.

82. (Amended) The article of manufacture of claim 81, wherein said medium is: a server, a hard drive, a CD-ROM or a diskette.